<110> The Regents of the University of California
Whistler, Jennifer L

<120> METHODS AND COMPOSITIONS FOR MODULATING AGONIST-INDUCED DOWNREGULATION OF G PROTEIN-COUPLED RECEPTORS

<130> 316E-001510US (12101-011-999)

<140> US/10/622,373
<141> 2003-07-18

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<170> PatentIn version 3.1

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Substitute Seq Listing 12101-011-999

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        435                 440                 445
Phe Gly Ser Trp Phe Trp Asp Arg Asp Glu Ala Cys Phe Asp Leu Asn
    450                 455                 460
Pro Cys Pro Val Tyr Lys Val Ser Asp Arg Phe Arg Asp Ala Ala Glu
465                 470                 475                 480
Glu Leu Asn Ala Ser Ser Arg Pro Gln Thr Trp Asp Glu Val Thr Val
                485                 490                 495
Glu Phe Lys Pro Gly Leu Phe His Gly Val Gly Phe Arg Ser Thr Ser
            500                 505                 510
Pro Phe Gly Ile Pro Glu Glu Ala Ser Glu Met Leu Glu Ala Lys Pro
        515                 520                 525
Lys Asn Leu Glu Leu Ser Pro Glu Gly Glu Glu Gln Glu Ser Leu Leu
    530                 535                 540
Gln Pro Asp Gln Pro Ser Pro Glu Phe Thr Phe Gln Tyr Asp Pro Ser
545                 550                 555                 560
Tyr Arg Ser Val Arg Glu Ile Arg Glu His Leu Arg Ala Arg Glu Ser
                565                 570                 575
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Ala Glu Ser Glu Ser Trp Ser Cys Ser Cys Ile Gln Cys Glu Leu Lys
580 585 590
Ile Gly Ser Glu Glu Phe Glu Glu Phe Leu Leu Leu Met Asp Lys Ile
595 600 605
Arg Asp Pro Phe Ile His Glu Ile Ser Lys Ile Ala Met Gly Met Arg
610 615 620
Ser Ala Ser Gln Phe Thr Arg Asp Phe Ile Arg Asp Ser Gly Val Val
625 630 635 640
Ser Leu Ile Glu Thr Leu Leu Asn Tyr Pro Ser Ser Arg Val Arg Thr
645 650 655
Ser Phe Leu Glu Asn Met Ile His Met Ala Pro Pro Tyr Pro Asn Leu
660 665 670
Asn Met Ile Glu Thr Phe Ile Cys Gln Val Cys Glu Glu Thr Leu Ala
675 680 685
His Ser Val Asp Ser Leu Glu Gln Leu Thr Gly Ile Arg Met Leu Arg
690 695 700
His Leu Thr Met Thr Ile Asp Tyr His Thr Leu Ile Ala Asn Tyr Met
705 710 715 720
Ser Gly Phe Leu Ser Leu Leu Thr Thr Ala Asn Ala Arg Thr Lys Phe
725 730 735
His Val Leu Lys Met Leu Leu Asn Leu Ser Glu Asn Pro Ala Val Ala
740 745 750
Lys Lys Leu Phe Ser Ala Lys Ala Leu Ser Ile Phe Val Gly Leu Phe
755 760 765
Asn Ile Glu Glu Thr Asn Asp Asn Ile Gln Ile Val Ile Lys Met Phe
770 775 780
Gln Asn Ile Ser Asn Ile Ile Lys Ser Gly Lys Met Ser Leu Ile Asp
785 790 795 800
Asp Asp Phe Ser Leu Glu Pro Leu Ile Ser Ala Phe Arg Glu Phe Glu
805 810 815
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Glu Val Gly Gln Gln Ser
835

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<212> PRT
<213> Artificial Sequence

<220>
<223> opioid peptide DADLE

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<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa = D-Ala

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa = D-Leu

<400> 7
Tyr Xaa Gly Phe Xaa
1 5

<210> 8
<211> 1491
<212> DNA
<213> Artificial Sequence

<220>
<223> coding sequence for cGASP1 (C-terminal 497 residues of GASP1).

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gaagaagcag gaccatgctg tgtatccaag ccagaggatg atgaagagat gattgttgag 120
tcctggttct ggtctagaga caaagccatt aaggaaactg gaactgtggc cacctgtgag 180
tccaagccag aaaatgagga aggggccatt gttgggtctt ggtttgaggc tgaagatgag 240
gtagataaca ggactgacaa tggaagcaac tgtgggtcca ggacattagc tgatgaagat 300
gaggccatag tggggtcctg gttctgggca ggagatgagg cccattttga atcaaatcct 360
agccccgtgt tcagggccat ttgcaggtcc acgtgttcag ttgaacagga gcctgatcct 420
tcacgcaggc ctcagagttg ggaggaggtc actgttcagt tcaagcctgg tccatggggt 480
agggtcggct tcccatctat aagccccttt agatttccga aagaggcagc atctttattc 540
tgtgaaatgt ttgggggcaa acccaggaac atggtactta gcccagaagg ggaagatcag 600
gaatctttgc ttcagcctga tcagcctagt cctgagttcc catttcagta tgatccttcc 660
tacaggtcag tccaggaaat tcgagagcat cttagggcca aggagagtac agagcctgag 720
agttcatcct gtaactgcat acaatgtgag ctgaaaattg gttctgaaga gtttgaagaa 780
ctccttttat taatggaaaa aattcgggat ccttttattc atgaaatatc taaaatcgca 840
atgggtatga gaagtgcttc tcaatttacc cgagatttca ttcgagattc aggtgttgtc 900
tcacttattg aaaccttgct taattatccg tcctcccgag ttagaacaag ttttttggaa 960
aatatgattc gcatggcccc accttatccg aatctaaaca taattcagac atacatatgt 1020
aaagtgtgtg aggaaaccct tgcttatagc gtggattccc cggaacagct gtctggaata 1080
aggatgatta gacatctcac tactactact gactatcaca cactggttgc caattatatg 1140
tctgggtttc tctccttatt agctacaggc aatgccaaaa caaggtttca tgttttgaaa 1200
atgctactga atttgtctga aaatcttttc atgacaaaag aactactcag tgctgaagca 1260
gtgtcagaat ttataggcct ctttaacagg gaagagacaa atgacaatat tcaaattgtt 1320
cttgcaatat ttgagaatat tggcaacaat atcaaaaaag aaacagtgtt ctctgatgat 1380
gatttcaata ttgagccgct tatttctgca ttccacaaag ttgagaaatt tgctaaggaa 1440
ctgcaaggca aaacagacaa tcaaaatgac cctgaagggg accaagaaaa t 1491

<210> 9
<211> 497
<212> PRT
<213> Artificial Sequence

<220>
<223> cGASP1 (C-terminal 497 residues of GASP1)

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Lys Glu Val Ser Glu Glu Ala Gly Pro Cys Cys Val Ser Lys Pro Glu
            20   25   30
Asp Asp Glu Glu Met Ile Val Glu Ser Trp Phe Trp Ser Arg Asp Lys
        35   40   45
Ala Ile Lys Glu Thr Gly Thr Val Ala Thr Cys Glu Ser Lys Pro Glu
    50   55   60
Asn Glu Glu Gly Ala Ile Val Gly Ser Trp Phe Glu Ala Glu Asp Glu
65   70   75   80
Val Asp Asn Arg Thr Asp Asn Gly Ser Asn Cys Gly Ser Arg Thr Leu
                85   90   95
Ala Asp Glu Asp Glu Ala Ile Val Gly Ser Trp Phe Trp Ala Gly Asp
            100   105   110
Glu Ala His Phe Glu Ser Asn Pro Ser Pro Val Phe Arg Ala Ile Cys
        115   120   125
Arg Ser Thr Cys Ser Val Glu Gln Glu Pro Asp Pro Ser Arg Arg Pro
    130   135   140
Gln Ser Trp Glu Glu Val Thr Val Gln Phe Lys Pro Gly Pro Trp Gly
145   150   155   160
Arg Val Gly Phe Pro Ser Ile Ser Pro Phe Arg Phe Pro Lys Glu Ala
                165   170   175
Ala Ser Leu Phe Cys Glu Met Phe Gly Gly Lys Pro Arg Asn Met Val
            180   185   190

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Leu Ser Pro Glu Gly Glu Asp Gln Glu Ser Leu Leu Gln Pro Asp Gln
        195                 200                 205
Pro Ser Pro Glu Phe Pro Phe Gln Tyr Asp Pro Ser Tyr Arg Ser Val
    210                 215                 220
Gln Glu Ile Arg Glu His Leu Arg Ala Lys Glu Ser Thr Glu Pro Glu
225                 230                 235                 240
Ser Ser Ser Cys Asn Cys Ile Gln Cys Glu Leu Lys Ile Gly Ser Glu
                245                 250                 255
Glu Phe Glu Glu Leu Leu Leu Leu Met Glu Lys Ile Arg Asp Pro Phe
            260                 265                 270
Ile His Glu Ile Ser Lys Ile Ala Met Gly Met Arg Ser Ala Ser Gln
        275                 280                 285
Phe Thr Arg Asp Phe Ile Arg Asp Ser Gly Val Val Ser Leu Ile Glu
    290                 295                 300
Thr Leu Leu Asn Tyr Pro Ser Ser Arg Val Arg Thr Ser Phe Leu Glu
305                 310                 315                 320
Asn Met Ile Arg Met Ala Pro Pro Tyr Pro Asn Leu Asn Ile Ile Gln
                325                 330                 335
Thr Tyr Ile Cys Lys Val Cys Glu Glu Thr Leu Ala Tyr Ser Val Asp
            340                 345                 350
Ser Pro Glu Gln Leu Ser Gly Ile Arg Met Ile Arg His Leu Thr Thr
        355                 360                 365
Thr Thr Asp Tyr His Thr Leu Val Ala Asn Tyr Met Ser Gly Phe Leu
    370                 375                 380
Ser Leu Leu Ala Thr Gly Asn Ala Lys Thr Arg Phe His Val Leu Lys
385                 390                 395                 400
Met Leu Leu Asn Leu Ser Glu Asn Leu Phe Met Thr Lys Glu Leu Leu
                405                 410                 415
Ser Ala Glu Ala Val Ser Glu Phe Ile Gly Leu Phe Asn Arg Glu Glu
            420                 425                 430
Thr Asn Asp Asn Ile Gln Ile Val Leu Ala Ile Phe Glu Asn Ile Gly
        435                 440                 445
Asn Asn Ile Lys Lys Glu Thr Val Phe Ser Asp Asp Phe Asn Ile
    450                 455                 460
Glu Pro Leu Ile Ser Ala Phe His Lys Val Glu Lys Phe Ala Lys Glu
465                 470                 475                 480
Leu Gln Gly Lys Thr Asp Asn Gln Asn Asp Pro Glu Gly Asp Gln Glu
                485                 490                 495
Asn
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